## CLAIM AMENDMENTS

1. *(Currently Amended)* A method of identifying a nucleic acid that encodes human telomerase reverse transcriptase (hTRT) or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to the nucleic acid if the nucleic acid encodes hTRT or fragment thereof;

b) detecting any hybrid formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the hybrid is detected;

wherein the probe hybridizes specifically to a DNA having the sequence of the hTRT encoding region of SEQ. ID NO:224 at 5°C to 25°C below $T_m$ in aqueous solution at 1 M NaCl but does not hybridize to a DNA having the sequence of SEQ. ID NO:62 under the same reaction conditions;

wherein $T_m$ is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.

2. *(Currently Amended)* A method of detecting a nucleic acid that encodes hTRT or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ. ID NO:224 if present in the sample;

b) detecting any hybrid formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the hybrid is detected;

wherein the polynucleotide probe consists essentially of a sequence identical or complementary to 25 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224 that are not contained in SEQ. ID NO:62.

3. *(Original)* The method of claim 2, wherein the hTRT nucleic acid is human genomic DNA.

4. *(Previously presented)* The method of claim 2, wherein the hTRT nucleic acid is mRNA or cDNA.

5. *(Previously presented)* The method of claim 2, wherein the hTRT nucleic acid consists essentially of 250 or more nucleotides of SEQ. ID NO:224.

6. *(Previously presented)* The method of claim 2, wherein the hTRT nucleic acid consists essentially of 500 or more nucleotides of SEQ. ID NO:224.

7. *(Previously presented)* The method of claim 2, wherein the probe consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224.

8. *(Previously presented)* The method of claim 2, wherein the probe consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224.

9. *(Previously presented)* The method of claim 2, wherein the probe consists essentially of a sequence identical or complementary to 100 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224.

10 to 12. *CANCELLED*

13. *(Currently Amended)* A method of identifying a nucleic acid that encodes hTRT or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide primer under conditions that the primer specifically primes amplification of SEQ. ID NO:224 or fragment thereof if present in the sample;

b) detecting any amplification product formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the amplification product is detected;

wherein the primer hybridizes specifically to a DNA having the sequence of the hTRT encoding region of SEQ. ID NO:224 at 5°C to 25°C below $T_m$ in aqueous solution at 1 M NaCl , but does not hybridize to a DNA having the sequence of SEQ. ID NO:62 under the same reaction conditions;

wherein $T_m$ is the melting temperature of double-stranded DNA having the sequence of said encoding region under the same reaction conditions.

14. *(Currently Amended)* A method of detecting a nucleic acid encoding hTRT or fragment thereof in a sample, comprising:

a) combining the sample with polynucleotide primers so as to prime amplification of nucleic acid encoding hTRT or fragment thereof if present in the sample;

b) detecting any amplified product formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the amplification product is detected;

wherein each of said primers consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224 , but

at least one of the primers does not consist of a sequence identical or complementary to 15 or more consecutive nucleotides from SEQ. ID NO:62.

15. *(Previously presented)* The method of claim 14, wherein each of said primers consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224.

16. *(Previously presented)* The method of claim 14, wherein each of said primers consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224.

17 to 22. *CANCELLED*

23. *(Withdrawn)* ~~A combination~~ A pair of oligonucleotide primers for PCR amplification for use in detecting an hTRT nucleic acid according to claim 14, wherein each primer consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224 , but at least one of the primers does not consist of a sequence identical or complementary to 15 or more consecutive nucleotides from SEQ. ID NO:62.

24 to 25. *CANCELLED*

26 to 34. *CANCELLED*

35. *(Previously presented)* The method of claim 1, wherein a) comprises combining the sample with the probe at 5°C to 25°C below $T_m$ in aqueous solution at 1 M NaCl.

36. *CANCELLED*

37. *(Previously presented)* The method of claim 1, wherein the probe comprises a sequence identical or complementary to 100 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224.

38. *CANCELLED.*

39. *(Previously presented)* The method of claim 1, wherein the sample has been taken from a patient having a tumor.

40. *(Previously presented)* The method of claim 2, wherein the sample has been taken from a patient having a tumor.

41. *(Previously presented)* The method of claim 13, wherein a) comprises combining the sample with the primer at 5°C to 25°C below $T_m$ in aqueous solution at 1 M NaCl.

42. *CANCELLED.*

43. *(Previously presented)* The method of claim 13, wherein the primer comprises a sequence identical or complementary to 30 or more consecutive nucleotides from the hTRT encoding region of SEQ. ID NO:224.

44. *CANCELLED*

45. *(Previously presented)* The method of claim 13, wherein the sample has been taken from a patient having a tumor.

46. *(Previously presented)* The method of claim 14, wherein the sample has been taken from a patient having a tumor.

47. *(New)* A method of identifying a nucleic acid that encodes human telomerase reverse transcriptase (hTRT) or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to the nucleic acid if the nucleic acid encodes hTRT or fragment thereof;

b) detecting any hybrid formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the hybrid is detected;

wherein the probe hybridizes specifically to a DNA having a sequence consisting of SEQ. ID NO:62 at 5°C to 25°C below $T_m$ in aqueous solution at 1 M NaCl;

wherein $T_m$ is the melting temperature of double-stranded DNA having the sequence of SEQ. ID NO:62 under the same reaction conditions.

48. *(New)* The method of claim 47, wherein a) comprises combining the sample with the probe at 5°C to 25°C below $T_m$ in aqueous solution at 1 M NaCl.

49. *(New)* The method of claim 47, wherein the probe comprises a sequence identical or complementary to 100 or more consecutive nucleotides from SEQ. ID NO:62.

50. *(New)* The method of claim 47, wherein the probe is a fragment of SEQ. ID NO:62.

51. *(New)* The method of claim 47, wherein the sample has been taken from a patient having a tumor.

52. *(New)* A method of detecting a nucleic acid that encodes hTRT or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes specifically to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ. ID NO:62 if present in the sample;

b) detecting any hybrid formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the hybrid is detected;

wherein the polynucleotide probe consists essentially of a sequence identical or complementary to 25 or more consecutive nucleotides from SEQ. ID NO:62.

53. *(New)* The method of claim 52, wherein the probe consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from SEQ. ID NO:62.

54. *(New)* The method of claim 52, wherein the probe consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from SEQ. ID NO:62.

55. *(New)* The method of claim 52, wherein the probe consists essentially of a sequence identical or complementary to 100 or more consecutive nucleotides from SEQ. ID NO:62.

56. *(New)* The method of claim 52, wherein the sample has been taken from a patient having a tumor.

57. *(New)* A method of identifying a nucleic acid that encodes hTRT or fragment thereof in a sample, comprising:

a) combining the sample with a polynucleotide primer under conditions that the primer specifically primes amplification of SEQ. ID NO:62 or fragment thereof if present in the sample;

b) detecting any amplification product formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the amplification product is detected;

wherein the primer hybridizes specifically to a DNA having a sequence consisting of SEQ. ID NO:62 at 5°C to 25°C below $T_m$ in aqueous solution at 1 M NaCl;

wherein $T_m$ is the melting temperature of double-stranded DNA having the sequence of SEQ. ID NO:62 under the same reaction conditions.

58. *(New)* The method of claim 57, wherein a) comprises combining the sample with the primer at 5°C to 25°C below $T_m$ in aqueous solution at 1 M NaCl.

59. *(New)* The method of claim 57, wherein the primer comprises a sequence identical or complementary to 30 or more consecutive nucleotides from SEQ. ID NO:62.

60. *(New)* The method of claim 57, wherein the probe is a fragment of SEQ. ID NO:62.

61. *(New)* The method of claim 57, wherein the sample has been taken from a patient having a tumor.

62. *(New)* A method of detecting a nucleic acid encoding hTRT or fragment thereof in a sample, comprising:

a) combining the sample with polynucleotide primers so as to prime amplification of nucleic acid encoding hTRT or fragment thereof if present in the sample;

b) detecting any amplified product formed as a result of a); and

c) identifying the nucleic acid as encoding hTRT or fragment thereof if the amplification product is detected;

wherein each of said primers consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from SEQ. ID NO:62.

63. *(New)* The method of claim 62, wherein each of said primers consists essentially of a sequence identical or complementary to 30 or more consecutive nucleotides from SEQ. ID NO:62.

64. *(New)* The method of claim 62, wherein each of said primers consists essentially of a sequence identical or complementary to 50 or more consecutive nucleotides from SEQ. ID NO:62.

65. *(New)* A pair of oligonucleotide primers for PCR amplification for use in detecting an hTRT nucleic acid according to claim 62, wherein each primer consists essentially of a sequence identical or complementary to 15 or more consecutive nucleotides from SEQ. ID NO:62.

66. *(New)* The method of claim 62, wherein the sample has been taken from a patient having a tumor.